RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/325,278*

DATE: 10/07/96
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1/8/97

This Raw Listing contains the General Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Bj-rck, Lars
Sj-bring, Ulf

(ii) TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: SEED and BERRY LLP
(B) STREET: 6300 Columbia Center, 701 Fifth Avenue
(C) CITY: Seattle
(D) STATE: Washington
(E) COUNTRY: USA
(F) ZIP: 98104-7092

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/325,278
(B) FILING DATE: 26-OCT-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: McMasters, David D.
(B) REGISTRATION NUMBER: 33,963
(C) REFERENCE/DOCKET NUMBER: 450023.401

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (206) 622-4900
(B) TELEFAX: (206) 682-6031

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Ala Val Glu Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser
1               5                  10                  15

Glu Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser
            20                  25                  30

Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu
        35                  40                  45

Ala Tyr Ala Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr
    50                  55                  60

Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
65                  70                  75                  80

Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
                85                  90                  95

Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
            100                 105                 110

Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
        115                 120                 125

Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
    130                 135                 140

Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro
145                 150                 155                 160

Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys
                165                 170                 175

Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu
            180                 185                 190

Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr
        195                 200                 205

Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
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100           210                 215                 220
101
102       Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
103       225                 230                 235                 240
104
105       Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
106                       245                 250                 255
107
108       Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
109                   260                 265                 270
110
111       Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
112               275                 280                 285
113
114       Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu
115           290                 295                 300
116
117       Glu
118       305
119
120   (2) INFORMATION FOR SEQ ID NO:2:
121
122        (i) SEQUENCE CHARACTERISTICS:
123             (A) LENGTH: 921 base pairs
124             (B) TYPE: nucleic acid
125             (C) STRANDEDNESS: double
126             (D) TOPOLOGY: unknown
127
128       (ii) MOLECULE TYPE: DNA (genomic)
129
130      (iii) HYPOTHETICAL: NO
131
132       (vi) ORIGINAL SOURCE:
133             (A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
134
135
136
137       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
138
139   GCGGTAGAAA ATAAAGAAGA AACACCAGAA ACACCAGAAA CTGATTCAGA AGAAGAAGTA      60
140
141   ACAATCAAAG CTAACCTAAT CTTTGCAAAT GGAAGCACAC AAACTGCAGA ATTCAAAGGA     120
142
143   ACATTTGAAA AAGCAACATC AGAAGCTTAT GCGTATGCAG ATACTTTGAA GAAAGACAAT     180
144
145   GGAGAATATA CTGTAGATGT TGCAGATAAA GGTTATACTT TAAATATTAA ATTTGCTGGA     240
146
147   AAAGAAAAAA CACCAGAAGA ACCAAAAGAA GAAGTTACTA TTAAAGCAAA CTTAATCTAT     300
148
149   GCAGATGGAA AAACACAAAC AGCAGAATTC AAAGGAACAT TTGAAGAAGC AACAGCAGAA     360
150
151   GCATACAGAT ATGCAGATGC ATTAAAGAAG GACAATGGAG AATATACAGT AGACGTTGCA     420
152
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GATAAAGGTT ATACTTTAAA TATTAAATTT GCTGGAAAAG AAAAAACACC AGAAGAACCA 480

AAAGAAGAAG TTACTATTAA AGCAAACTTA ATCTATGCAG ATGGAAAAAC ACAAACAGCA 540

GAATTCAAAG GAACATTTGA AGAAGCAACA GCAGAAGCAT ACAGATATGC TGACTTATTA 600

GCAAAAGAAA ATGGTAAATA TACAGTAGAC GTTGCAGATA AAGGTTATAC TTTAAATATT 660

AAATTTGCTG GAAAAGAAAA AACACCAGAA GAACCAAAAG AAGAAGTTAC TATTAAAGCA 720

AACTTAATCT ATGCAGATGG AAAAACTCAA ACAGCAGAGT TCAAAGGAAC ATTTGCAGAA 780

GCAACAGCAG AAGCATACAG ATACGCTGAC TTATTAGCAA AAGAAAATGG TAAATATACA 840

GCAGACTTAG AAGATGGTGG ATACACTATT AATATTAGAT TTGCAGGTAA GAAAGTTGAC 900

GAAAAACCAG AAGAATAATA A 921

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 434 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Ala Val Glu Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser
1               5                  10                  15

Glu Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser
            20                  25                  30

Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu
        35                  40                  45

Ala Tyr Ala Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr
    50                  55                  60

Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
65                  70                  75                  80

Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
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                    85                  90                  95

Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
            100                 105                 110

Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
        115                 120                 125

Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
    130                 135                 140

Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro
145                 150                 155                 160

Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys
                165                 170                 175

Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu
            180                 185                 190

Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr
        195                 200                 205

Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
    210                 215                 220

Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
225                 230                 235                 240

Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
                245                 250                 255

Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
            260                 265                 270

Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
        275                 280                 285

Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu
    290                 295                 300

Glu Pro Met Asp Thr Tyr Lys Leu Ile Leu Asn Gly Lys Thr Leu Lys
305                 310                 315                 320

Gly Glu Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val
                325                 330                 335

Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr
            340                 345                 350

Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile
        355                 360                 365
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